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- (71) Applicant (for all designated States except US): **CEN-
TRE FOR ADDICTION AND MENTAL HEALTH**
[CA/CA]; 33 Russell Street, Toronto, Ontario M5S 2S1
(CA).

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- (72) Inventor; and
- (75) Inventor/Applicant (for US only): **PETRONIS, Arturas**
[CA/CA]; 250 College Street, Toronto, Ontario M5T 1R8
(CA).

- (74) Agents: **GOWLING LAFLEUR HENDERSON LLP** et al.; 160 Elgin Street, Suite 2600, Ottawa, Ontario K1P 1C3 (CA).

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(54) Title: **DETECTION OF EPIGENETIC ABNORMALITIES AND DIAGNOSTIC METHOD BASED THEREON**

Sch74-E52m/Sch74-E51m CAGCTCACTGCAACCTCCGCC-TCTTGGATTCAAGC-GATTTCCTGGCTTAC-CCTCTGAGTAAGTGGGACTAGAGGACAGGACACCCAGCTAAATTTT-GTATT
BD43-E78m/BD43-E83m OGCTCAATGCAACCTCAGCC-TCTTGGGTTCAAGC-AATTCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
BD43-E78m CGGCTCAATGCAACCTCAGCC-TCTTGGGTTCAAGC-AATTCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
BD34-D19m TGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGT-AATTCTCTGCTCTCAG-CCTCTGAGTAGCTAGGATTACTGGTGCCGCCACCATGCCCCGCAATTTT-GTATT
BD34-E52m TGCTCACTGCAACCTCAGC-TCTTGGGTTCAAGT-AATTCTCTGCTCTCAG-CCTCTGAGTAGCTAGGATTACTGGTGCCGCCACCATGCCCCGCAATTTT-GTATT
BD34-E52m TGCTCACTGCAACCTCAGC-TCTTGGGTTCAAGC-GATTCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Ctt157-E53m CAGCTCACTGCAACCTCCATT-TCTTGGGTTCAAGC-GATTCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
BD43-RevE7m CAGCTCACTGCAACCTCCACC-TCTTGGGTTCAAGT-GATTATCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
BD43-RevE77m CAGCTCACTGCAACCTCCACC-TCTTGGGTTCAAGT-GATTATCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
BD34-A14M CGGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGC-GATTCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Ctt157-E53m TGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGC-AATTCTCTGCTCTCAG-TCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Sch74-E318m TGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGC-AATTCTCTGCTCTCAG-TCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Ctt157-E54m TGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGC-AATTCTCTGCTCTCAG-TCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
BD43-E79m CAGCTCACTGCAACCTCCGCT-TCTTGGGTTCAAGC-AATTCTCTGCTCTCAG-TCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Ctt157-E56m CAGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGC-GATTCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Ctt157-E56m CAGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGC-GATTCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Ctt150-RevE169m CAGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGC-GATTCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Sch56-E283m CAGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGT-GATTCTCTGCTCTGAT-CCTACCAAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Sch56-r-37m CAGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGT-GATTCTCTGCTCTGAT-CCTACCAAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Sch56-E32m CAGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGT-GATTCTCTGCTCTGAT-CCTACCAAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Ctt150-E166m CGGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGC-AATTCTCTGCTCTCAG-CCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT
Ctt150-E49m CGGCTCACTGCAACCTCCGCC-TCTTGGGTTCAAGC-GATTCTCTGCTCTCAGCTCCGAGTAGCTGGGATTACAGGCACATGCCCACTGCCAACTAAATTTT-GTATT

(57) Abstract: The present invention provides a method of detecting an epigenetic abnormality associated with a disease. The method comprises identifying, within a eukaryotic genome, a locus having a hypomethylated sequence specific for the disease and an endogenous multi-copy DNA element. The method can also comprise separate steps of identifying a disease-specific hypomethylated sequence and identifying an endogenous multi-copy DNA element, where the steps may be performed in any order, so long as a locus is identified that has both a disease-specific hypomethylated sequence and an endogenous multi-copy DNA element. The disease-specific hypomethylated sequences detected in accordance with the present invention indicate putative regions of epigenetic dys-regulation and indicate aberrantly regulated nucleic acid sequences that may cause or predispose a patient to disease, such as, but not limited to, Huntingdon s disease, cancers, diabetes, schizophrenia, or bipolar disorder.

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